<u>VisIt</u> is a free interactive parallel visualization and graphical analysis tool for viewing scientific data on Unix and PC platforms. It is widely used in various DOE labs and for other large simulations. <u>VisIt</u> has developed an ITAPS_MOAB reader that can be used to view .h5m (HDF5) and .cub(CUBIT) files.

Follow these steps to build <u>VisIt</u> with ITAPS option:

- 1. Goto: http://portal.nersc.gov/svn/visit/trunk/releases/2.3.0/build_visit2_3_0 (This version has been tested and installed, you can try the latest one)
- 2. Copy the shell script in a file and save it as build_visit.sh in an empty folder. Make it an executable with chmod +x build visit.sh.

If you have configured PyTAPS, you may have used the home scheme, in which the local ~/.pydistutils.cfg was edited to define the "home" installation folder for python bindings on your local machine. (http://trac.mcs.anl.gov/projects/ITAPS/wiki/InstallingPyTAPS). You need to disable that file while you are building https://trac.mcs.anl.gov/projects/ITAPS/wiki/InstallingPyTAPS). You need to

- 3. Invoke the script 'build_visit.sh'.
- 4. Choose 'Advanced' on the installation window, select ITAPS, NETCDF and HDF5 options. You may choose other options like Silo, Exodus.
- 5. It will take a while, it will build and install several packages it needs and finally will build <u>VisIt</u>.
- 6. You can also launch the build script with a command like

```
./build_visit.sh --itaps --python --console --hdf5 --netcdf --exodus --szip --silo
```

7. All done, now cd into the visit2.3.0/src/bin directory and launch visit - './visit'. You can add <visit2.3.0/src/bin>to your PATH variable, or you can follow the

installation instructions to install it in a different folder.

Note: gcc-4.4.3 and g++-4.4.3 were used to build this version.

When opening an .h5m file make sure to use 'Open file as type' as 'ITAPS_MOAB', otherwise you will get an error message.